SEQUENCE LISTING

ATTATUS 40 44

- (1) GENERAL INFORMATION:
 - (i) APPLICANT: Gary S. Gray et al.
 - (ii) TITLE OF INVENTION: CTLA-4-C74 Fusion Proteins (As Amended)
 - (iii) NUMBER OF SEQUENCES: 32
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: LAHIVE & COCKFIELD
 - (B) STREET: 28 State Street
 - (C) CITY: Boston
 - (D) STATE: Massachusetts
 - (E) COUNTRY: USA
 - (F) ZIP: 02109-1875
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: Not yet available
 - (B) FILING DATE: December 20, 2001
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/227,595
 - (B) FILING DATE: January 8, 1999
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Amy E. Mandragouras
 - (B) REGISTRATION NUMBER: 36,207
 - (C) REFERENCE/DOCKET NUMBER: RPN-001CN
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617)227-7400
 - (B) TELEFAX: (617)227-5941
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CATTCTAGAA CCTCGACAAG CTTGAGATCA CAGTTCTCTC TAC	43
(2) INFORMATION FOR SEQ ID NO:2:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 46 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
CAGCAGGCTG GGCCACGTGC ATTGCGGAGT GGACACCTGT GGAGAG	46
(2) INFORMATION FOR SEQ ID NO:3:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 46 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: CTCTCCACAG GTGTCCACTC CGCAATGCAC GTGGCCCAGC CTGCTG	46
(2) INFORMATION FOR SEQ ID NO:4:	40
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 46 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
TGTGTGTGGA ATTCTCATTA CTGATCAGAA TCTGGGCACG GTTCTG	46
(2) INFORMATION FOR SEQ ID NO:5:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 78 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
GCATTTTAAG CTTTTTCCTG ATCAGGAGCC CAAATCTTCT GACAAAACTC ACACATCTCC	6
ACCGTCTCCA GGTAAGCC	7
(2) INFORMATION FOR SEQ ID NO:6:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
TAATACGACT CACTATAGGG	20
(2) INFORMATION FOR SEQ ID NO:7:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 66 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	
GAGCATTTTC CTGATCAGGA GTCCAAATAT GGTCCCCCAC CCCATCATCC CCAGGTAAGC	60
CAACCC	66
(2) INFORMATION FOR SEQ ID NO:8:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 68 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO.8:	

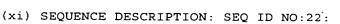
GCAGAGGAAT TCGAGCTCGG TACCCGGGGA TCCCCAGTGT GGGGACAGTG GGACCCGCTC	60
TGCCTCCC	68
(2) INFORMATION FOR SEQ ID NO:9:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 59 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:	
GGGTTTTGGG GGGAAGAGGA AGACTGACGG TGCCCCCTCG GCTTCAGGTG CTGAGGAAG	59
(2) INFORMATION FOR SEQ ID NO:10:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 56 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:	
CATCTCTTCC TCAGCACCTG AAGCCGAGGG GGCACCGTCA GTCTTCCTCT TCCCCC	56
(2) INFORMATION FOR SEQ ID NO:11:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 99 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:	
CGCACGTGAC CTCAGGGGTC CGGGAGATCA TGAGAGTGTC CTTGGGTTTT GGGGGGAACA	60
GGAAGACTGA TGGTGCCCCC TCGAACTCAG GTGCTGAGG	99
(2) INFORMATION FOR SEQ ID NO:12:	

	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 99 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	
CCTC	CAGCACC TGAGTTCGAG GGGGCACCAT CAGTCTTCCT GTTCCCCCCA AAACCCAAGG	60
ACAC	CTCTCAT GATCTCCCGG ACCCCTGAGG TCACGTGCG	99
(2)	INFORMATION FOR SEQ ID NO:13:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 43 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:	
CATT	CGCTTA CCTCGACAAG CTTGAGATCA CAGTTCTCTC TAC	43
(2)	INFORMATION FOR SEQ ID NO:14:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:	
GGAG	ETGGACA CCTGTGGAGA G	21
(2)	INFORMATION FOR SEQ ID NO:15:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:	
CTCCACAGGT GTCCACTCCG CAATGCACGT GGCCCAGCC	3.9
(2) INFORMATION FOR SEQ ID NO:16:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:	
GAGGTTGTAA GGACTCACCT GAAATCTGGG CTCCGTTGC	39
(2) INFORMATION FOR SEQ ID NO:17:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:	
GCAACGGAGC CCAGATTTCA GGTGAGTCCT TACAACCTC	39
(2) INFORMATION FOR SEQ ID NO:18:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 39 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	~•
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:	
GGCTAGATAT CTCTAGACTA TAAATCTCTG GCCATGAAG	39
(2) INFORMATION FOR SEQ ID NO:19:	
(') 07077707 07777777	

(A) LENGTH: 73 base pairs(B) TYPE: nucleic acid

<pre>(C) STRANDEDNESS: single (D) TOPOLOGY: linear</pre>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:	
GGCACTAGGT CGACTCTAGA AACTGAGGAA GCAAAGTTTA AATTCTACTC ACGTTTAATC	50
TGGGCTCCGT TGC	73
(2) INFORMATION FOR SEQ ID NO:20:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 43 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:	
GCAGAGAGAC ATATGGCAAT GCACGTGGCC CAGCCTGCTG TGG	3
(2) INFORMATION FOR SEQ ID NO:21:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:	
GCAGAGAGA GATCCTCAGT CAGTTAGTCA GAATCTGGGC ACGGTTCTGG 5	0
(2) INFORMATION FOR SEQ ID NO:22:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 107 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	



GGCACTAGTC	ATGAAATACC	TATTGCCTAC	GGCAGCCGCT	GGATTGTTAT	TACTCGCTGC	6 (
CCAACCAGCG	ATGGCCGCAG	CAATGCACGT	GGCCCAGCCT	GCTGTGG		10

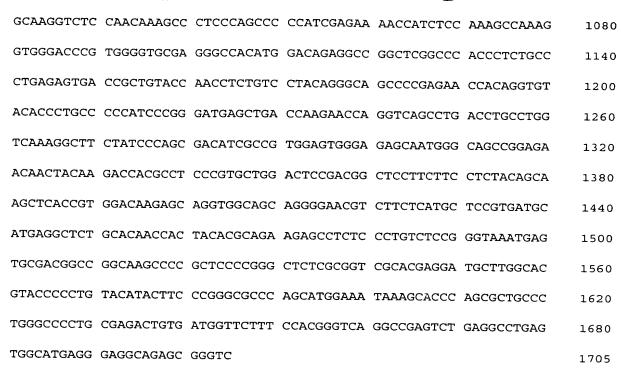
(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1705 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CATTCGCTTA	CCTCGAGAAG	CTTGAGATCA	CAGTTCTCTC	TACAGTTACT	GAGCACACAG	60
GACCTCACCA	TGGGATGGAG	CTGTATCATC	CTCTTCTTGG	TAGCAACAGC	TACAGGTAAG	120
GGGCTCACAG	TAGCAGGCTT	GAGGTCTGGA	CATATATATG	GGTGACAATG	ACATCCACTT	180
TGCCTTTCTC	TCCACAGGTG	TCCACTCCGC	AATGCACGTG	GCCCAGCCTG	CTGTGGTACT	240
GGCCAGCAGC	CGAGGCATCG	CCAGCTTTGT	GTGTGAGTAT	GCATCTCCAG	GCAAAGCCAC	300
TGAGGTCCGG	GTGACAGTGC	TTCGGCAGGC	TGACAGCCAG	GTGACTGAAG	TCTGTGCGGC	360
AACCTACATG	ATGGGGAATG	AGTTGACCTT	CCTAGATGAT	TCCATCTGCA	CGGGCACCTC	420
CAGTGGAAAT	CAAGTGAACC	TCACTATCCA	AGGACTGAGG	GCCATGGACA	CGGGACTCTA	480
CATCTGCAAG	GTGGAGCTCA	TGTACCCACC	GCCATACTAC	CTGGGCATAG	GCAACGGAAC	540
CCAGATTTAT	GTAATTGATC	CAGAACCGTG	CCCAGATTCT	GATCAGGAGC	CCAAATCTTC	600
TGACAAAACT	CACACATCTC	CACCGTCTCC	AGGTAAGCCA	GCCCAGGCCT	CGCCCTCCAG	660
CTCAAGGCGG	GACAGGTGCC	CTAGAGTAGC	CTGCATCCAG	GGACAGGCCC	CAGCCGGGTG	720
CTGACACGTC	CACCTCCATC	TCTTCCTCAG	CACCTGAAGC	CGAGGGGGCA	CCGTCAGTCT	780
TCCTCTTCCC	CCCAAAACCC	AAGGACACCC	TCATGATCTC	CCGGACCCCT	GAGGTCACAT	840
GCGTGGTGGT	GGACGTGAGC	CACGAAGACC	CTGAGGTCAA	GTTCAACTGG	TACGTGGACG	900
GCGTGGAGGT	GCATAATGCC	AAGACAAAGC	CGCGGGAGGA	GCAGTACAAC	AGCACGTACC	960
GGGTGGTCAG	CGTCCTCACC	GTCCTGCACC	AGGACTGGCT	GAATGGCAAG	GAGTACAAGT	1020



(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 377 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Gly Tfp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 10 15

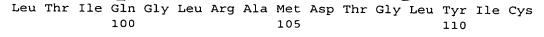
Val His Ser Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser 20 25 30

Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys 35 40 45

Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val 50 60

Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe 70 75 80

Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn 85 90 95



Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn 115 120 125

Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp 130 135 140

Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro 145 150 155 160

Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys 165 170 175

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val 180 185 190

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr 195 200 205

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu 210 215 220

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His 225 230 235 240

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys 245 250 255

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln 260 265 270

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu 275 280 285

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro 290 295 300

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn 305 4 310 315 320

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu 325 330 335

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val 340 345 350

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln 355 360 365

Lys Ser Leu Ser Leu Ser Pro Gly Lys 370 375

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1747 base pairs

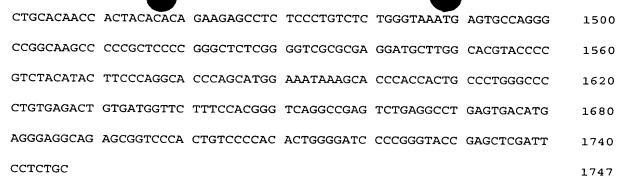


- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CATTCGCTTA CCTCGAGAAG CTTGAGATCA CAGTTCTCTC TACAGTTACT GAGCACACAG 60 GACCTCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTAAG 120 GGGCTCACAG TAGCAGGCTT GAGGTCTGGA CATATATATG GGTGACAATG ACATCCACTT 180 TGCCTTTCTC TCCACAGGTG TCCACTCCGC AATGCACGTG GCCCAGCCTG CTGTGGTACT 240 GGCCAGCAGC CGAGGCATCG CCAGCTTTGT GTGTGAGTAT GCATCTCCAG GCAAAGCCAC 300 TGAGGTCCGG GTGACAGTGC TTCGGCAGGC TGACAGCCAG GTGACTGAAG TCTGTGCGGC 360 AACCTACATG ATGGGGAATG AGTTGACCTT CCTAGATGAT TCCATCTGCA CGGGCACCTC 420 CAGTGGAAAT CAAGTGAACC TCACTATCCA AGGACTGAGG GCCATGGACA CGGGACTCTA 480 CATCTGCAAG GTGGAGCTCA TGTACCCACC GCCATACTAC CTGGGCATAG GCAACGGAAC 540 CCAGATTTAT GTAATTGATC CAGAACCGTG CCCAGATTCT GATCAGGAGT CCAAATATGG 600 TCCCCCATCC CCATCATCCC CAGGTAAGCC AACCCAGGCC TCGCCCTCCA GCTCAAGGCG 660 GGACAGGTGC CCTAGAGTAG CCTGCATCCA GGGACAGGCC CCAGCCGGGT GCTGACGCAT 720 CCACCTCCAT CTCTTCCTCA GCACCTGAGT TCCTGGGGGG ACCATCAGTC TTCCTGTTCC 780 CCCCAAAACC CAAGGACACT CTCATGATCT CCCGGACCCC TGAGGTCACG TGCGTGGTGG 840 TGGACGTGAG CCAGGAAGAC CCCGAGGTCC AGTTCAACTG GTACGTGGAT GGCGTGGAGG 900 TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTTCAA CAGCACGTAC CGTGTGGTCA 960 GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAACGGCAA GGAGTACAAG TGCAAGGTCT 1020 CCAACAAGG CCTCCCGTCC TCCATCGAGA AAACCATCTC CAAAGCCAAA GGTGGGACCC 1080 ACGGGGTGCG AGGGCCACAC GGACAGAGGC CAGCTCGGCC CACCCTCTGC CCTGGGAGTG 1140 ACCGCTGTGC CAACCTCTGT CCCTACAGGG CAGCCCCGAG AGCCACAGGT GTACACCCTG 1200 CCCCCATCCC AGGAGGAGAT GACCAAGAAC CAGGTCAGCC TGACCTGCCT GGTCAAAGGC 1260 TTCTACCCCA GCGACATCGC CGTGGAGTGG GAGAGCAATG GGCAGCCGGA GAACAACTAC 1320 AAGACCACGC CTCCCGTGCT GGACTCCGAC GGCTCCTTCT TCCTCTACAG CAGGCTAACC 1380 GTGGACAAGA GCAGGTGGCA GGAGGGGAAT GTCTTCTCAT GCTCCGTGAT GCATGAGGCT 1440



(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 374 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:
 - Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15
 - Val His Ser Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser 20 25 30
 - Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys 35 40 45
 - Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val 50 60
 - Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe 65 70 75 80
 - Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn 85 90 95
 - Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys 100 105 110
 - Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn 115 120 125
 - Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp 130 135 140

 - Phe Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp 165 170 175

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp 180 185 190

Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
195 200 205

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn 210 215 220

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp 225 230 235 240

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
245 250 255

Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu 260 265 270

Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn 275 280 285

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile 290 295 300

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Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg 325 330 335

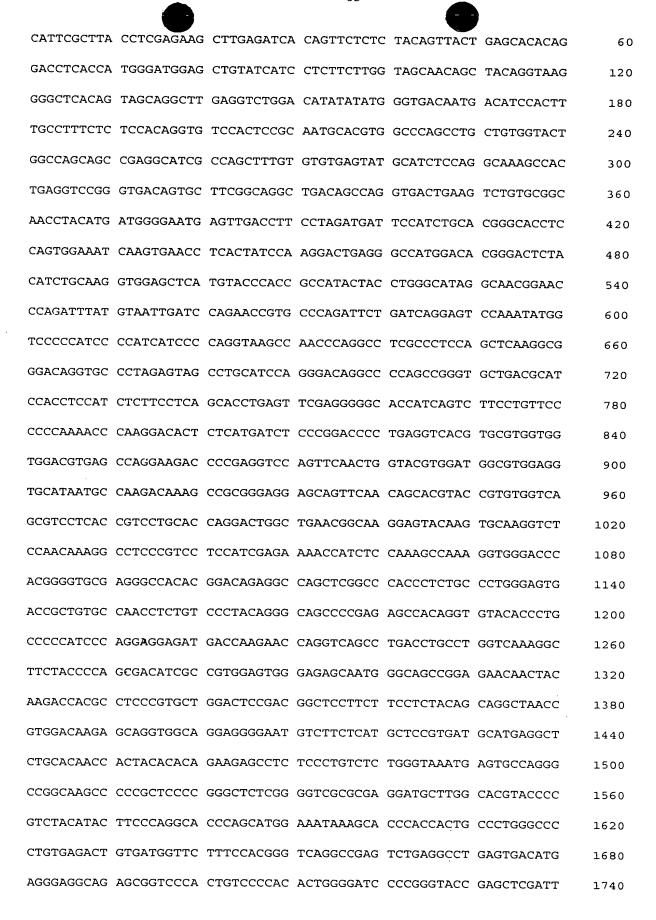
Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys 340 345 350

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu 355 360 365

Ser Leu Ser Leu Gly Lys 370

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1747 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:



CCTCTGC 1747

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 374 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser 20 25 30

Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys 35 40 45

Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val 50 55 60

Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe 70 75 80

Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn 85 90 95

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Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn 115 120 125

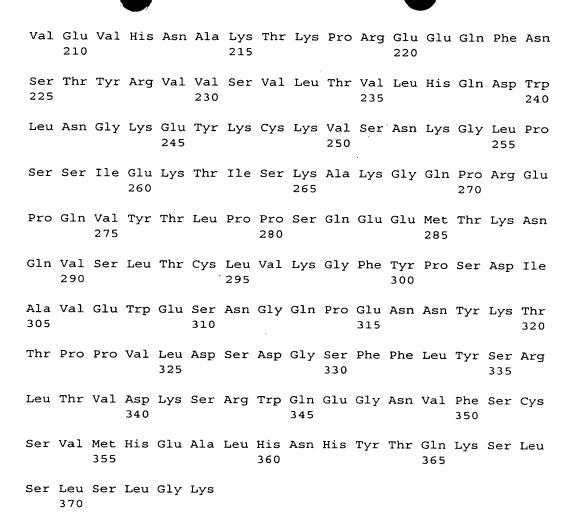
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Gln Glu Ser Lys Tyr Gly Pro Pro Ser Pro Ser Pro Ala Pro Glu 145 150 155 160

Phe Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp 165 170 175

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Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
195 200 205

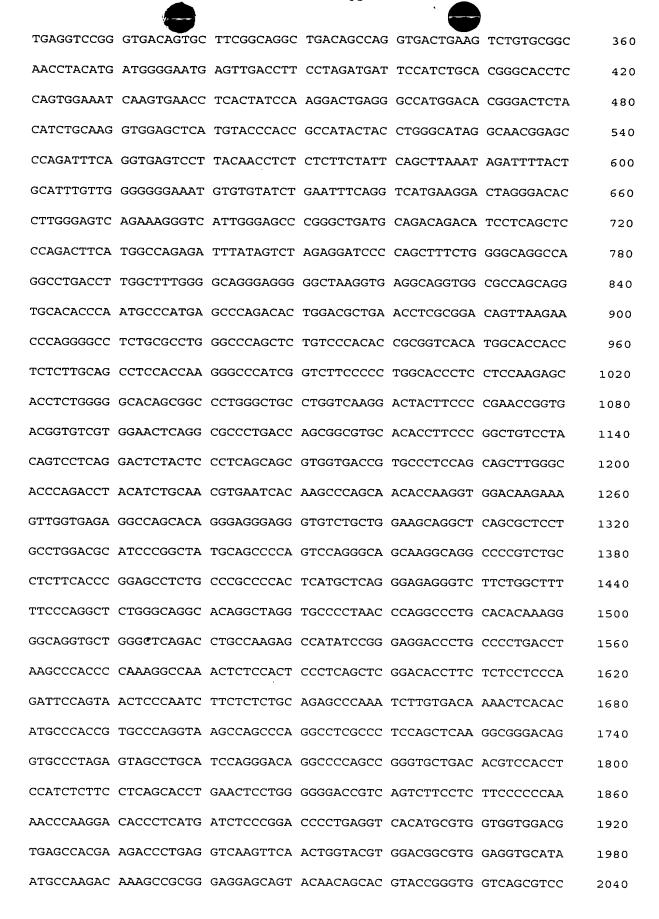


(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2770 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLĖCULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CATTCGCTTA	CCTCGAGAAG	CTTGAGATCA	CAGTTCTCTC	TACAGTTACT	GAGCACACAG	60
GACCTCACCA	TGGGATGGAG	CTGTATCATC	CTCTTCTTGG	TAGCAACAGC	TACAGGTAAG	120
GGGCTCACAG	TAGCAGGCTT	GAGGTCTGGA	CATATATATG	GGTGACAATG	ACATCCACTT	180
TGCCTTTCTC	TCCACAGGTG	TCCACTCCGC	AATGCACGTG	GCCCAGCCTG	CTGTGGTACT	240
GGCCAGCAGC	CGAGGCATCG	CCAGCTTTGT	GTGTGAGTAT	GCATCTCCAG	GCAAAGCCAC	300





(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 238 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
 - (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

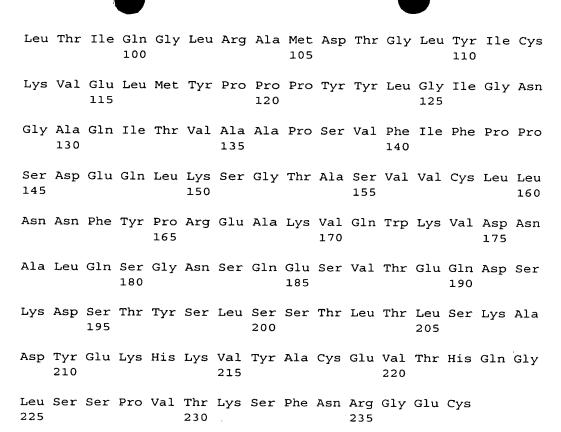
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Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys 35 40 45

Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val 50 60

Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe 65 70 75 80

Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn 85 90 95



(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1708 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CATTCGCTTA	CĊTCGAGAAG	CTTGAGATCA	CAGTTCTCTC	TACAGTTACT	GAGCACACAG	60
GACCTCACCA	TGGGATGGAG	CTGTATCATC	CTCTTCTTGG	TAGCAACAGC	TACAGGTAAG	120
GGGCTCACAG	TAGCAGGCTT	GAGGTCTGGA	CATATATATG	GGTGACAATG	ACATCCACTT	180
TGCCTTTCTC	TCCACAGGTG	TCCACTCCGC	AATGCACGTG	GCCCAGCCTG	CTGTGGTACT	240
GGCCAGCAGC	CGAGGCATCG	CCAGCTTTGT	GTGTGAGTAT	GCATCTCCAG	GCAAAGCCAC	300
TGAGGTCCGG	GTGACAGTGC	TTCGGCAGGC	TGACAGCCAG	GTGACTGAAG	TCTGTGCGGC	360
AACCTACATG	ATGGGGAATG	AGTTGACCTT	CCTAGATGAT	TCCATCTGCA	CGGGCACCTC	420
CAGTGGAAAT	CAAGTGAACC	TCACTATCCA	AGGACTGAGG	GCCATGGACA	CGGGACTCTA	480



(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 238 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly

Val His Ser Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser

Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys 40

Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val 55

Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe 75

Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn

Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys 105

Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn 120

Gly Ala Gln Ile Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro 135

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn 165 170

Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser 185

Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly 215

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys